

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Susan DYMECKI

(ii) TITLE OF INVENTION: Use of Flp Recombinase in Mice

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

(B) STREET: 1100 New York Avenue, N.W.

(C) CITY: Washington

(D) STATE: D.C.

(E) COUNTRY: USA

(F) ZIP: 20005-3918

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: Microsoft Word

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGTGAAAGT TCCTATTCCG AAGTTCTAT TCTCTAGAAA GTATAGGAAC

50

TTCCCTAGGA GATTCGAA GGCTCGAGC

79

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TAGCTACGTA GAAGTTCTTA TTCCGAAGTT CCTATTCTCT AGAAAAGTATA 50  
GGAACTTCA 59

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTAGGGAAAGT TCCTATACTT TCTAGAGAAT AGGAACCTCG GAATAGGAAC 50  
TTCA 100

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCGGTGAAAGT TCCTATACTT TCTAGAGAAT AGGAACCTCG GAATAGGAAC 50  
TTCTACGTAG CTAGCTCGAG CCTTCGAAGA TCTC 84

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTAAGGTACC GGTGAAGTTC CTA

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCACCCACC GGTGAAGTTC CTA

23

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTACCGAGC TCAGCCACCA TGACTGCTCC AAAGAAGAAC CGTAAGGTAC	50
CGGTGAAGTT CCTATTCCGA AGTTCTTATT CTCTAGAAAG TATAGGAACT	100
TCACCGGTGG GTGAAGACCA GAAACAGCAC CTCGAACCTGA GCCGCGATAT	150
TGCCCAGCGT TTCAACGCGC TGTATGGCGA GATCGATCCC GTCGTTTAC	200
AACGTCGTGA C	211

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Ala Pro Lys Lys Lys Arg Lys Val Pro Val Lys Phe Leu  
1 5 10 15

Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr Ser Pro Val  
20 25 30

Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp Ile Ala  
35 40 45

Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile Asp Pro Val Val Leu  
50 55 60

Gln Arg Arg Asp

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Pro Lys Lys Lys Arg Lys Val  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Phe Leu Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr  
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Pro Val Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp  
1 5 10 15

Ile Ala Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile  
20 25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

C 1

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAAGTTCTTA TTC 13

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAAGTTCCTA TAC

13

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC

34

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAAGTTCCTA TTCCGAAGTT CCTATTCTCT AGAAAGTATA GGAACCTTC

48

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGCCACAAT TTGATATATT ATGTAAAACA CCACCTAAGG TGCTTGTCG TCAGTTGTG 60

GAAAGGTTTG AAAGACCTTC AGGTGAGAAA ATAGCATTAT GTGCTGCTGA ACTAACCTAT 120

TTATGTTGGA TGATTACACA TAACCGAACCA GCAATCAAGA GAGCCACATT CATGAGCTAT 180

AATACTATCA TAAGCAATTG GCTGAGTTG GATATTGTCA ACAAGTCACT GCAGTTAAA 240

a1

TACAAGACGC AAAAAGCAAC AATTCTGGAA GCCTCATTAA AGAAATTGAT TCCTGCTTGG 300  
 GAATTTACAA TTATTCCTTA CTATGGACAA AAACATCAAT CTGATATCAC TGATATTGTA 360  
 AGTAGTTGC AATTACAGTT CGAACATCATCG GAAGAAGCAG ATAAGGGAAA TAGCCACAGT 420  
 AAAAAAAATGC TTAAAGCACT TCTAAGTGAG GGTGAAAGCA TCTGGGAGAT CACTGAGAAA 480  
 ATACTAAATT CGTTGAGTA TACTTCGAGA TTTACAAAAA CAAAAACTTT ATACCAATT 540  
 CTCTTCCTAG CTACTTCAT CAATTGTGGA AGATTACAGCG ATATTAAGAA CGTTGATCCG 600  
 AAATCATTAA AATTAGTCCA AAATAAGTAT CTGGGAGTAA TAATCCAGTG TTTAGTGACA 660  
 GAGACAAAGA CAAGCGTTAG TAGGCACATA TACTTCTTTA GCGCAAGGGG TAGGATCGAT 720  
 CCACTTGTAT ATTTGGATGA ATTTTGAGG AATTCTGAAC CAGTCCTAAA ACGAGTAAAT 780  
 AGGACCGGCA ATTCTTCAAG CAACAAGCAG GAATACCAAT TATTAAGA TAACTTAGTC 840  
 AGATCGTACA ACAAAAGCTT GAAGAAAAAT GCGCCTTATT CAATCTTGC TATAAAAAT 900  
 GGCCCCAAAT CTCACATTGG AAGACATTG ATGACCTCAT TTCTTCAAT GAAGGGCCTA 960  
 ACGGAGTTGA CTAATGTTGT GGGAAATTGG AGCGATAAGC GTGCTTCTGC CGTGGCCAGG 1020  
 ACAACGTATA CTCATCAGAT AACAGCAATA CCTGATCACT ACTTCGCACT AGTTTCTCGG 1080  
 TACTATGCAT ATGATCCAAT ATCAAAGGAA ATGATAGCAT TGAAGGATGA GACTAATCCA 1140  
 ATTGAGGAGT GGCAGCATA AGAACAGCTA AAGGGTAGTG CTGAAGGAAG CATAKGATAC 1200  
 CCCGCATGGA ATGGGATAAT ATCACAGGAG GTACTAGACT ACCTTTCATC CTACATAAAAT 1260  
 AGACGCATAT AA 1272

(a)

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Pro	Gln	Phe	Asp	Ile	Leu	Cys	Lys	Thr	Pro	Pro	Lys	Val	Leu
1														15
Val	Arg	Gln	Phe	Val	Glu	Arg	Phe	Glu	Arg	Pro	Ser	Gly	Glu	Lys
				20				25						30
Ile	Ala	Leu	Cys	Ala	Ala	Glu	Leu	Thr	Tyr	Leu	Cys	Trp	Met	Ile
				35				40						45
Thr	His	Asn	Gly	Thr	Ala	Ile	Lys	Arg	Ala	Thr	Phe	Met	Ser	Tyr
				50				55						60

Asn	Thr	Ile	Ile	Ser	Asn	Ser	Leu	Ser	Leu	Asp	Ile	Val	Asn	Lys
					65					70				75
Ser	Leu	Gln	Phe	Lys	Tyr	Lys	Thr	Gln	Lys	Ala	Thr	Ile	Leu	Glu
				80					85					90
Ala	Ser	Leu	Lys	Lys	Leu	Ile	Pro	Ala	Trp	Glu	Phe	Thr	Ile	Ile
				95					100					105
Pro	Tyr	Tyr	Gly	Gln	Lys	His	Gln	Ser	Asp	Ile	Thr	Asp	Ile	Val
				110					115					120
Ser	Ser	Leu	Gln	Leu	Gln	Phe	Glu	Ser	Ser	Glu	Glu	Ala	Asp	Lys
				125					130					135
Gly	Asn	Ser	His	Ser	Lys	Lys	Met	Leu	Lys	Ala	Leu	Leu	Ser	Glu
				140					145					150
Gly	Glu	Ser	Ile	Trp	Glu	Ile	Thr	Glu	Lys	Ile	Leu	Asn	Ser	Phe
				155					160					165
Glu	Tyr	Thr	Ser	Arg	Phe	Thr	Lys	Thr	Lys	Thr	Leu	Tyr	Gln	Phe
				170					175					180
Leu	Phe	Leu	Ala	Thr	Phe	Ile	Asn	Cys	Gly	Arg	Phe	Ser	Asp	Ile
				185					190					195
Lys	Asn	Val	Asp	Pro	Lys	Ser	Phe	Lys	Leu	Val	Gln	Asn	Lys	Tyr
				200					205					210
Leu	Gly	Val	Ile	Ile	Gln	Cys	Leu	Val	Thr	Glu	Thr	Lys	Thr	Ser
				215					220					225
Val	Ser	Arg	His	Ile	Tyr	Phe	Phe	Ser	Ala	Arg	Gly	Arg	Ile	Asp
				230					235					240
Pro	Leu	Val	Tyr	Leu	Asp	Glu	Phe	Leu	Arg	Asn	Ser	Glu	Pro	Val
				245					250					255
Leu	Lys	Arg	Val	Asn	Arg	Thr	Gln	Asn	Ser	Ser	Ser	Asn	Lys	Gln
				260					265					270
Glu	Tyr	Gln	Leu	Leu	Lys	Asp	Asn	Leu	Val	Arg	Ser	Tyr	Asn	Lys
				275					280					285
Ala	Leu	Lys	Lys	Asn	Ala	Pro	Tyr	Ser	Ile	Phe	Ala	Ile	Lys	Asn
				290					295					300
Gly	Pro	Lys	Ser	His	Ile	Gly	Arg	His	Leu	Met	Thr	Ser	Phe	Leu
				305					310					315
Ser	Met	Lys	Gly	Leu	Thr	Glu	Leu	Thr	Asn	Val	Val	Gly	Asn	Trp
				320					325					330
Ser	Asp	Lys	Arg	Ala	Ser	Ala	Val	Ala	Arg	Thr	Thr	Tyr	Thr	His
				335					340					345
Gln	Ile	Thr	Ala	Ile	Pro	Asp	His	Tyr	Phe	Ale	Leu	Val	Ser	Arg
				350					355					360
Tyr	Tyr	Ala	Tyr	Asp	Pro	Ile	Ser	Lys	Glu	Met	Ile	Ala	Leu	Lys
				365					370					375

Asp	Glu	Thr	Asn	Pro	Ile	Glu	Glu	Trp	Gln	His	Ile	Glu	Gln	Leu
						380			385					390
Lys	Gly	Ser	Ala	Glu	Gly	Ser	Ile	Arg	Tyr	Pro	Ala	Trp	Asn	Gly
						395			400					405
Ile	Ile	Ser	Gln	Glu	Val	Leu	Asp	Tyr	Leu	Ser	Ser	Tyr	Ile	Asn
						410			415					420
Arg	Arg	Ile												

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGCCACAAT	TTGATATATT	ATGTAAAACA	CCACCTAAGG	TGCTTGTTCG	TCAGTTGTG	60
GAAAGGTTG	AAAGACCTTC	AGGTGAGAAA	ATAGCATTAT	GTGCTGCTGA	ACTAACCTAT	120
TTATGTTGGA	TGATTACACA	TAACGGAACA	GCAATCAAGA	GAGCCACATT	CATGAGCTAT	180
AATACTATCA	TAAGCAATTTC	GCTGAGTTTC	GATATTGTCA	ACAAGTCACT	GCAGTTAAA	240
TACAAGACGC	AAAAAGCAAC	AATTCTGGAA	GCCTCATTAA	AGAAATTGAT	TCCTGCTTGG	300
GAATTACAA	TTATTCCTTA	CTATGGACAA	AAACATCAAT	CTGATATCAC	TGATATTGTA	360
AGTAGTTGC	AATTACAGTT	CGAACATCG	GAAGAACGAG	ATAAGGGAAA	TAGCCACAGT	420
AAAAAAATGC	TTAAAGCACT	TCTAAGTGAG	GGTGAAAGCA	TCTGGGAGAT	CACTGAGAAA	480
ATACTAAATT	CGTTTGAGTA	TACTTCGAGA	TTTACAAAAA	CAAAACTTT	ATACCAATT	540
CTCTTCCTAG	CTACTTTCAT	CAATTGTGGA	AGATTCAAGCG	ATATTAAGAA	CGTTGATCCG	600
AAATCATTAA	AATTAGTCCA	AAATAAGTAT	CTGGGAGTAA	TAATCCAGTG	TTTAGTGACA	660
GAGACAAAGA	CAAGCGTTAG	TAGGCACATA	TACTTCTTA	GCGCAAGGGG	TAGGATCGAT	720
CCACTTGTAT	ATTTGGATGA	ATTTTGAGG	AATTCTGAAC	CAGTCCTAAA	ACGAGTAAAT	780
AGGACCGGCA	ATTCTTCAAG	AAACAAGCAG	GAATACCAAT	TATTAAGA	TAACCTAGTC	840
AGATCGTACA	ACAAAGCTT	GAAGAAAAAT	GCGCCTTATT	CAATCTTGC	TATAAAAAT	900
GGCCCAAAAT	CTCACATTGG	AAAGACATTG	ATGACCTCAT	TTCTTCAAT	GAAGGCCCTA	960
ACGGAGTTGA	CTAATGTTGT	GGGAAATTGG	AGCGATAAGC	GTGCTTCTGC	CGTGGCCAGG	1020
ACAACGTATA	CTCATCAGAT	AAACAGCAATA	CCTGATCACT	ACTTCGCACT	AGTTTCTCGG	1080

TACTATGCAT ATGATCCAAT ATCAAAGGAA ATGATAGCAT TGAAGGATGA GACTAATCCA 1140  
ATTGAGGAGT GGCAGCATAT AGAACAGCTA AAGGGTAGTG CTGAAGGAAG CATAcgATAC 1200  
CCCGCATGGA ATGGGATAAT ATCACAGGAG GTACTAGACT ACCTTTCATC CTACATAAAT 1260  
AGACGCATAT AA 1272

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu  
1 5 10 15

Val Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys  
20 25 30

Ile Ala Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile  
35 40 45

Thr His Asn Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr  
50 55 60

Asn Thr Ile Ile Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys  
65 70 75

Ser Leu Gln Phe Lys Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu  
80 85 90

Ala Ser Leu Lys Lys Leu Ile Pro Ala Trp Glu Phe Thr Ile Ile  
95 100 105

Pro Tyr Tyr Gly Gln Lys His Gln Ser Asp Ile Thr Asp Ile Val  
110 115 120

Ser Ser Leu Gln Leu Gln Phe Glu Ser Ser Glu Glu Ala Asp Lys  
125 130 135

Gly Asn Ser His Ser Lys Lys Met Leu Lys Ala Leu Leu Ser Glu  
140 145 150

Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys Ile Leu Asn Ser Phe  
155 160 165

Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr Leu Tyr Gln Phe  
170 175 180

Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe Ser Asp Ile  
185 190 195

G1

Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn Lys Tyr  
 200 205 210  
 Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr Ser  
 215 220 225  
 Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp  
 230 235 240  
 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val  
 245 250 255  
 Leu Lys Arg Val Asn Arg Thr Gln Asn Ser Ser Ser Asn Lys Gln  
 260 265 270  
 Glu Tyr Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys  
 275 280 285  
 Ala Leu Lys Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn  
 290 295 300  
 Gly Pro Lys Ser His Ile Gly Arg His Leu Met Thr Ser Phe Leu  
 305 310 315  
 Ser Met Lys Gly Leu Thr Glu Leu Thr Asn Val Val Gly Asn Trp  
 320 325 330  
 Ser Asp Lys Arg Ala Ser Ala Val Ala Arg Thr Thr Tyr Thr His  
 335 340 345  
 Gln Ile Thr Ala Ile Pro Asp His Tyr Phe Ale Leu Val Ser Arg  
 350 355 360  
 Tyr Tyr Ala Tyr Asp Pro Ile Ser Lys Glu Met Ile Ala Leu Lys  
 365 370 375  
 Asp Glu Thr Asn Pro Ile Glu Glu Trp Gln His Ile Glu Gln Leu  
 380 385 390  
 Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr Pro Ala Trp Asn Gly  
 395 400 405  
 Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser Ser Tyr Ile Asn  
 410 415 420  
 Arg Arg Ile

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGTCCAAGTG CAGGCCAAGC TTCC

24

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGGATCGAT CCTACCCCTT GCG

23

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACTGCTCCA AAGAAGAAC GTAAGG

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCTATTACGC CAGCTGGCGA AAGG

24